

SEQUENCE LISTING

<110> Fraunhofer Gesellschaft zur Förderung der angewandten
 Forschung e.V.
 <120> Immunokinases
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 <140> PCT/EP2005/050131
 <141> 2005-01-13
 <150> 04000847.6
 <151> 2004-01-16
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 <151> 2004-07-29
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 open reading frame (ORF)

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 <222> (1)..(21)
 <223> immunoglobulin kappa chain leader sequence

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aat atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att	144
Asn Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile	
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Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg	
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gag aag agc acg ggg ctg gag tat gca gcc aag ttc att aag aag agg	240
Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg	
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cag agc cgg gcc agc cgt cgg ggc gtg tgc cgg gag gaa atc gag cgg	288
Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg	
85 90 95	
gag gtg agc atc ctg cgg cag gtg ctg cac ccc aac atc atc acg ctg	336
Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu	
100 105 110	

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Val	Ser	Gly	Gly	Glu	Leu	Phe	Asp	Phe	Leu	Ala	Gln	Lys	Glü	Ser	Leu	
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Ile	Asp	Phe	Gly	Leu	Ala	His	Glu	Ile	Glu	Asp	Gly	Val	Glu	Phe	Lys	
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Tyr	Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln	
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gaa	acc	ctg	gca	aat	atc	act	gct	gtg	agt	tac	gac	ttt	gat	gag	gaa	816
Glu	Thr	Leu	Ala	Asn	Ile	Thr	Ala	Val	Ser	Tyr	Asp	Phe	Asp	Glu	Glu	
							260		265				270			
ttc	ttc	agc	cag	aca	agc	gag	ctg	gcc	aag	gac	ttc	att	cg	aag	ctt	864
Phe	Phe	Ser	Gln	Thr	Ser	Glu	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Lys	Leu	
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ctt	gtg	aaa	gag	acc	cgg	aaa	cgg	ctt	acc	atc	caa	gag	gct	ctc	aga	912
Leu	Val	Lys	Glu	Thr	Arg	Lys	Arg	Leu	Thr	Ile	Gln	Glu	Ala	Leu	Arg	
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Thr	Phe	Thr	Asp	Tyr	Trp	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	
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ggt tca ggc gga ggt ggc tct ggc ggt ggc gga tcg gac att gtg ctg Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Asp Ile Val Leu 450 455 460	1392
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35 40 45

Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg
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Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg
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Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg
85 90 95

Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu
100 105 110

His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu
115 120 125

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Ser Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val
145 150 155 160

Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu
165 170 175

Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu
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Ile Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys
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Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr
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Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr
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Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln
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Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu
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Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu
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Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg
290 295 300

His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala
305 310 315 320

His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala
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340 345 350

Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln
355 360 365

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr Thr Asp
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Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser
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Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser
405 410 415

Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp Gly Phe
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Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
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450 455 460

Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg Val Thr
465 470 475 480

Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser Trp Tyr
485 490 495

Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser
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Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly Ser Gly
515 520 525

Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala
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Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe Gly Ala
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ggt tcc act ggt gac gcg gcc cag ccg gcc atg gcc cag gtc aag ctg	96
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu	
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cag gag tca ggg act gaa ctg gca aag cct ggg gcc gca gtg aag atg	144
Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met	
35 40 45	
tcc tgc aag gct tct ggc tac acc ttt act gac tac tgg atg cac tgg	192
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp	
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gtt aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att aat	240
Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn	
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Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala	
85 90 95	
aca ttg act gca gac aaa tcc tcc agc aca gcc tac atg caa ctg cgc	336
Thr Leu Thr Ala Asp Lys Ser Ser Thr Ala Tyr Met Gln Leu Arg	
100 105 110	
agc ctg acc tct gag gat tct gca gtc tat tac tgt gca aaa aag aca	384
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr	
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gcc gca ctc gag tct aga atg gtc cag gcc tcg atg agg agc cca aat Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn 275 280 285				864
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cca ctg gga ctg gag gcc gac atg tgg agc att gga gtc atc acc tat Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr	1488
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Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met
35 40 45

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp
Page 8

50

55

60

Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
65 70 75 80

Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala
85 90 95

Thr Leu Thr Ala Asp Lys Ser Ser Thr Ala Tyr Met Gln Leu Arg
100 105 110

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr
115 120 125

Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val
130 135 140

Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met
165 170 175

Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val
180 185 190

Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
195 200 205

Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
210 215 220

Phe Ala Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser
225 230 235 240

Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg
245 250 255

Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala
260 265 270

Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn
275 280 285

Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
290 295 300

Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu
305 310 315 320

Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln
325 330 335

Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg Glu
340 345 350

Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu His
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Asp Leu Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu Val
370 375 380

Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser
385 390 395 400

Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn
405 410 415

Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn
420 425 430

Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile
435 440 445

Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn
450 455 460

Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
465 470 475 480

Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
485 490 495

Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu
500 505 510

Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu Phe
515 520 525

Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu
530 535 540

Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His
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Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Phe Arg Gly Gly Pro
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His His His His His
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Ala Gln Pro Ala Met Ala Met Gly His His His His His His His His		
20 25 30		
cat cac agc agc ggc cat atc gac gac gac aag cat atg aag ctt		144
His His Ser Ser Gly His Ile Asp Asp Asp Asp Lys His Met Lys Leu		
35 40 45		
atg gcc cag ccg gcc atg gcc cag gtc aag ctg cag gag tca ggg act		192
Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr		
50 55 60		
gaa ctg gca aag cct ggg gcc gca gtg aag atg tcc tgc aag gct tct		240
Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser		
65 70 75 80		
ggc tac acc ttt act gac tac tgg atg cac tgg gtt aaa cag agg cct		288
Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro		
85 90 95		
gga cag ggt ctg gaa tgg att gga tac att aat cct aac act gct tat		336
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr		
100 105 110		
act gac tac aat cag aaa ttc aag gac aag gcc aca ttg act gca gac		384
Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp		
115 120 125		
aaa tcc tcc agc aca gcc tac atg caa ctg cgc agc ctg acc tct gag		432
Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu		
130 135 140		
gat tct gca gtc tat tac tgt gca aaa aag aca act cag act acg tgg		480
Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp		
145 150 155 160		
ggg ttt cct ttt tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt		528
Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly		
165 170 175		
gga ggc ggt tca ggc gga ggt ggc tct ggc ggt ggc gga tcg gac att		576
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile		
180 185 190		
gtg ctg acc cag tct cca aaa tcc atg gcc atg tca gtc gga gag agg		624

Val	Leu	Thr	Gln	Ser	Pro	Lys	Ser	Met	Ala	Met	Ser	Val	Gly	Glu	Arg	
195				200				205								
gtc	acc	ttg	agc	tgc	aag	gcc	agt	gag	aat	gtg	gat	tct	ttt	gtt	tcc	672
Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Ser	Phe	Val	Ser	
210				215				220								
tgg	tat	caa	cag	aaa	cca	ggc	cag	tct	cct	aaa	ctg	ctg	ata	tac	ggg	720
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	
225				230				235							240	
gcc	tcc	aac	cgg	tac	act	ggg	gtc	ccc	gat	cgc	ttc	gca	ggc	agt	gga	768
Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Ala	Gly	Ser	Gly	
245				250				255								
tct	gga	aga	gat	ttc	act	ctg	acc	atc	agc	agt	gtg	cag	gct	gaa	gac	816
Ser	Gly	Arg	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	
260				265				270								
ctt	gca	gat	tat	cac	tgt	gga	cag	aat	tac	agg	tat	ccg	ctc	acg	tcc	864
Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln	Asn	Tyr	Arg	Tyr	Pro	Leu	Thr	Phe	
275				280				285								
ggg	gct	ggc	acc	aag	ctg	gaa	atc	aaa	cgg	gcg	gcc	gca	gag	ctc	ggc	912
Gly	Ala	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Glu	Leu	Gly	
290				295				300								
gga	ggt	ggc	tct	atg	gca	gac	gaa	gat	ctc	atc	ttc	cgc	ctg	gaa	ggc	960
Gly	Gly	Gly	Ser	Met	Ala	Asp	Glu	Asp	Leu	Ile	Phe	Arg	Leu	Glu	Gly	
305				310				315							320	
gtt	gat	ggc	ggc	cag	tcc	ccc	cga	gct	ggc	cat	gat	ggt	gat	tct	gat	1008
Val	Asp	Gly	Gly	Gln	Ser	Pro	Arg	Ala	Gly	His	Asp	Gly	Asp	Ser	Asp	
325				330				335								
ggg	gac	agc	gac	gat	gag	gaa	ggt	tac	ttc	atc	tgc	ccc	atc	acg	gat	1056
Gly	Asp	Ser	Asp	Asp	Glu	Glu	Gly	Tyr	Phe	Ile	Cys	Pro	Ile	Thr	Asp	
340				345				350								
gac	cca	agc	tcg	aac	cag	aat	gtc	aat	tcc	aag	gtt	aat	aag	tac	tac	1104
Asp	Pro	Ser	Ser	Asn	Gln	Asn	Val	Asn	Ser	Lys	Val	Asn	Lys	Tyr	Tyr	
355				360				365								
agc	aac	cta	aca	aaa	agt	gag	cgg	tat	agc	tcc	agc	ggg	tcc	ccg	gca	1152
Ser	Asn	Leu	Thr	Lys	Ser	Glu	Arg	Tyr	Ser	Ser	Ser	Gly	Ser	Pro	Ala	
370				375				380								
aac	tcc	tcc	cac	tcc	aag	gaa	gcc	tgg	aag	cac	gca	atc	cag	aag	gcc	1200
Asn	Ser	Phe	His	Phe	Lys	Glu	Ala	Trp	Lys	His	Ala	Ile	Gln	Lys	Ala	
385				390				395							400	
aag	cac	atg	ccc	gac	ccc	tgg	gct	gag	ttc	cac	ctg	gaa	gat	att	gcc	1248
Lys	His	Met	Pro	Asp	Pro	Trp	Ala	Glu	Phe	His	Leu	Glu	Asp	Ile	Ala	
405				410				415								
acc	gaa	cgt	gct	act	cga	cac	agg	tac	aac	gcc	gtc	acc	ggg	gaa	tgg	1296
Thr	Glu	Arg	Ala	Thr	Arg	His	Arg	Tyr	Asn	Ala	Val	Thr	Gly	Glu	Trp	
420				425				430								
ctg	gat	gat	gaa	gtt	ctg	atc	aag	atg	gca	tct	cag	ccc	ttc	ggc	cga	1344
Leu	Asp	Asp	Glu	Val	Leu	Ile	Lys	Met	Ala	Ser	Gln	Pro	Phe	Gly	Arg	
435				440				445								
gga	gca	atg	agg	gag	tgc	ttc	cgg	acg	aag	aag	ctc	tcc	aac	ttc	ttg	1392
Gly	Ala	Met	Arg	Glu	Cys	Phe	Arg	Thr	Lys	Lys	Leu	Ser	Asn	Phe	Leu	
450				455				460								
cat	gcc	cag	cag	tgg	aag	ggc	gcc	tcc	aac	tac	gtg	gcg	aag	cgc	tac	1440
His	Ala	Gln	Gln	Trp	Lys	Gly	Ala	Ser	Asn	Tyr	Val	Ala	Lys	Arg	Tyr	

465	470	475	480	
atc gag ccc gta gac cg ^g gat gtg tac ttt gag gac gtg cgt cta cag Ile Glu Pro Val Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln 485 490 495				1488
atg gag gcc aag ctc tgg ggg gag gag tat aat cgg cac aag ccc ccc Met Glu Ala Lys Leu Trp Gly Glu Glu Tyr Asn Arg His Lys Pro Pro 500 505 510				1536
aag cag gtg gac atc atg cag atg tgc atc atc gag ctg aag gac aga Lys Gln Val Asp Ile Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg 515 520 525				1584
ccg ggc aag ccc ctc ttc cac ctg gag cac tac atc gag ggc aag tac Pro Gly Lys Pro Leu Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr 530 535 540				1632
atc aag tac aac tcc aac tct ggc ttt gtc cgc gat gac aac atc cgc Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg 545 550 555				1680
ctg acg ccg cag gcc ttc agc cac ttc act ttt gag cgt tcc ggc cat Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His 565 570 575				1728
cag ctg ata gtg gtg gac atc cag gga gtt ggg gat ctc tac act gac Gln Leu Ile Val Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp 580 585 590				1776
cca cag atc cac acg gag acg ggc act gac ttt gga gac ggc aac cta Pro Gln Ile His Thr Glu Thr Gly Thr Asp Phe Gly Asp Gly Asn Leu 595 600 605				1824
ggt gtc cgc ggg atg gcg ctc ttc tac tct cat gcc tgc aac cgg Gly Val Arg Gly Met Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg 610 615 620				1872
att tgc gag agc atg ggc ctt gct ccc ttt gac ctc tcg ccc cgg gag Ile Cys Glu Ser Met Gly Leu Ala Pro Phe Asp Leu Ser Pro Arg Glu 625 630 635 640				1920
agg gat gca gtg aat cag aac acc aag ctg ctg caa tca gcc aag acc Arg Asp Ala Val Asn Gln Asn Thr Lys Leu Leu Gln Ser Ala Lys Thr 645 650 655				1968
atc ttg aga gga aca gag gaa aaa tgt ggg agc ccc cga gta agg acc Ile Leu Arg Gly Thr Glu Glu Lys Cys Gly Ser Pro Arg Val Arg Thr 660 665 670				2016
ctc tct ggg agc cgg cca ccc ctg ctc cgt ccc ctt tca gag aac tct Leu Ser Gly Ser Arg Pro Pro Leu Leu Arg Pro Leu Ser Glu Asn Ser 675 680 685				2064
gga gac gag aac atg agc gac gtg acc ttc gac tct ctc cct tct tcc Gly Asp Glu Asn Met Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser 690 695 700				2112
cca tct tcg gcc aca cca cac agc cag aag cta gac cac ctc cat tgg Pro Ser Ser Ala Thr Pro His Ser Gln Lys Leu Asp His Leu His Trp 705 710 715 720				2160
cca gtc ttc agt gac ctc gat aac atg gca tcc aga gac cat gat cat Pro Val Phe Ser Asp Leu Asp Asn Met Ala Ser Arg Asp His Asp His 725 730 735				2208
cta gac aac cac cgg gag tct gag aat agt ggg gac agc gga tac ccc Leu Asp Asn His Arg Glu Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro 740 745 750				2256

agt	gag	aag	cgg	ggt	gag	ctg	gat	gac	cct	gag	ccc	cga	gaa	cat	ggc		2304
Ser	Glu	Lys	Arg	Gly	Glu	Leu	Asp	Asp	Pro	Glu	Pro	Arg	Glu	His	Gly		
755						760					765						
cac	tca	tac	agt	aat	cgg	aag	tac	gag	tct	gac	gaa	gac	agc	ctg	ggc		2352
His	Ser	Tyr	Ser	Asn	Arg	Lys	Tyr	Glu	Ser	Asp	Glu	Asp	Ser	Leu	Gly		
770						775					780						
agc	tct	gga	cgg	gta	tgt	gta	gag	aag	tgg	aat	ctc	ctc	aac	tcc	tcc		2400
Ser	Ser	Gly	Arg	Val	Cys	Val	Glu	Lys	Trp	Asn	Leu	Leu	Asn	Ser	Ser		
785						790				795					800		
cgc	ctc	cac	ctg	ccg	agg	gct	tcg	gcc	gtg	gcc	ctg	gaa	gtg	caa	agg		2448
Arg	Leu	His	Leu	Pro	Arg	Ala	Ser	Ala	Val	Ala	Leu	Glu	Val	Gln	Arg		
				805					810						815		
ctt	aat	gct	ctg	gac	ctc	gaa	aag	aaa	atc	ggg	aag	tcc	att	ttg	ggg		2496
Leu	Asn	Ala	Leu	Asp	Leu	Glu	Lys	Lys	Ile	Gly	Lys	Ser	Ile	Leu	Gly		
				820				825					830				
aag	gtc	cat	ctg	gcc	atg	gtg	cgc	tac	cac	gag	gtt	ggg	cgc	tcc	tgc		2544
Lys	Val	His	Leu	Ala	Met	Val	Arg	Tyr	His	Glu	Gly	Gly	Arg	Phe	Cys		
				835			840				845						
gag	aag	ggc	gag	gag	tgg	gac	cag	gag	tcg	gct	gtc	ttc	cac	ctg	gag		2592
Glu	Lys	Gly	Glu	Glu	Trp	Asp	Gln	Glu	Ser	Ala	Val	Phe	His	Leu	Glu		
				850		855				860							
cac	gca	gcc	aac	ctg	ggc	gag	ctg	gag	gcc	atc	gtg	ggc	ctg	gga	ctc		2640
His	Ala	Ala	Asn	Leu	Gly	Glu	Leu	Glu	Ala	Ile	Val	Gly	Leu	Gly	Leu		
				865		870			875						880		
atg	tac	tcg	cag	ttg	cct	cat	cac	atc	cta	gcc	gat	gtc	tct	ctg	aag		2688
Met	Tyr	Ser	Gln	Leu	Pro	His	His	Ile	Leu	Ala	Asp	Val	Ser	Leu	Lys		
				885				890					895				
gag	aca	gaa	gag	aac	aaa	acc	aaa	gga	ttt	gat	tac	tta	cta	aag	gcc		2736
Glu	Thr	Glu	Glu	Asn	Lys	Thr	Lys	Gly	Phe	Asp	Tyr	Leu	Leu	Lys	Ala		
				900				905				910					
gct	gaa	gct	ggc	gac	agg	cag	tcc	atg	atc	cta	gtg	gcg	cga	gct	ttt		2784
Ala	Glu	Ala	Gly	Asp	Arg	Gln	Ser	Met	Ile	Leu	Val	Ala	Arg	Ala	Phe		
				915			920				925						
gac	tct	ggc	cag	aac	ctc	agc	ccg	gac	agg	tgc	caa	gac	tgg	cta	gag		2832
Asp	Ser	Gly	Gln	Asn	Leu	Ser	Pro	Asp	Arg	Cys	Gln	Asp	Trp	Leu	Glu		
				930		935				940							
gcc	ctg	cac	tgg	tac	aac	act	gcc	ctg	gag	atg	acg	gac	tgt	gat	gag		2880
Ala	Leu	His	Trp	Tyr	Asn	Thr	Ala	Leu	Glu	Met	Thr	Asp	Cys	Asp	Glu		
				945		950				955					960		
ggc	ggt	gag	tac	gac	gga	atg	cag	gac	gag	ccc	cgg	tac	atg	atg	ctg		2928
Gly	Gly	Glu	Tyr	Asp	Gly	Met	Gln	Asp	Glu	Pro	Arg	Tyr	Met	Met	Leu		
				965				970				975					
gcc	agg	gag	gcc	gag	atg	ctg	ttc	aca	gga	ggc	tac	ggg	ctg	gag	aag		2976
Ala	Arg	Glu	Ala	Glu	Met	Leu	Phe	Thr	Gly	Gly	Tyr	Gly	Leu	Glu	Lys		
				980				985				990					
gac	ccg	cag	aga	tca	ggg	gac	ttg	tat	acc	cag	gca	gca	gag	gca	gcg		3024
Asp	Pro	Gln	Arg	Ser	Gly	Asp	Leu	Tyr	Thr	Gln	Ala	Ala	Glu	Ala	Ala		
				995			1000					1005					
atg	gaa	gcc	atg	aag	ggc	cga	ctg	gcc	aac	cag	tac	tac	caa	aag			3069
Met	Glu	Ala	Met	Lys	Gly	Arg	Leu	Ala	Asn	Gln	Tyr	Tyr	Gln	Lys			
				1010			1015				1020						

gct gaa gag gcc tgg gcc cag atg gag gag taa
Ala Glu Glu Ala Trp Ala Gln Met Glu Glu
1025 1030

3102

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<211> 1033
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 6

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Ala Gln Pro Ala Met Ala Met Gly His His His His His His His His
20 25 30

His His Ser Ser Gly His Ile Asp Asp Asp Asp Lys His Met Lys Leu
35 40 45

Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr
50 55 60

Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser
65 70 75 80

Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro
85 90 95

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr
100 105 110

Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp
115 120 125

Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu
130 135 140

Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp
145 150 155 160

Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
165 170 175

Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Asp Ile
180 185 190

Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg
195 200 205

Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser
210 215 220

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly
225 230 235 240

Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly
245 250 255

Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp
260 265 270

Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe
275 280 285

Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Leu Gly
290 295 300

Gly Gly Gly Ser Met Ala Asp Glu Asp Leu Ile Phe Arg Leu Glu Gly
305 310 315 320

Val Asp Gly Gly Gln Ser Pro Arg Ala Gly His Asp Gly Asp Ser Asp
325 330 335

Gly Asp Ser Asp Asp Glu Glu Gly Tyr Phe Ile Cys Pro Ile Thr Asp
340 345 350

Asp Pro Ser Ser Asn Gln Asn Val Asn Ser Lys Val Asn Lys Tyr Tyr
355 360 365

Ser Asn Leu Thr Lys Ser Glu Arg Tyr Ser Ser Ser Gly Ser Pro Ala
370 375 380

Asn Ser Phe His Phe Lys Glu Ala Trp Lys His Ala Ile Gln Lys Ala
385 390 395 400

Lys His Met Pro Asp Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala
405 410 415

Thr Glu Arg Ala Thr Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp
420 425 430

Leu Asp Asp Glu Val Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg
435 440 445

Gly Ala Met Arg Glu Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu
450 455 460

His Ala Gln Gln Trp Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr
465 470 475 480

Ile Glu Pro Val Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln
485 490 495

Met Glu Ala Lys Leu Trp Gly Glu Glu Tyr Asn Arg His Lys Pro Pro
500 505 510

Lys Gln Val Asp Ile Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg
515 520 525

Pro Gly Lys Pro Leu Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr
530 535 540

Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg
545 550 555 560

Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His
565 570 575

Gln Leu Ile Val Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp
580 585 590

Pro Gln Ile His Thr Glu Thr Gly Thr Asp Phe Gly Asp Gly Asn Leu
595 600 605

Gly Val Arg Gly Met Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg
610 615 620

Ile Cys Glu Ser Met Gly Leu Ala Pro Phe Asp Leu Ser Pro Arg Glu
625 630 635 640

Arg Asp Ala Val Asn Gln Asn Thr Lys Leu Leu Gln Ser Ala Lys Thr
645 650 655

Ile Leu Arg Gly Thr Glu Glu Lys Cys Gly Ser Pro Arg Val Arg Thr
660 665 670

Leu Ser Gly Ser Arg Pro Pro Leu Leu Arg Pro Leu Ser Glu Asn Ser
675 680 685

Gly Asp Glu Asn Met Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser
690 695 700

Pro Ser Ser Ala Thr Pro His Ser Gln Lys Leu Asp His Leu His Trp
705 710 715 720

Pro Val Phe Ser Asp Leu Asp Asn Met Ala Ser Arg Asp His Asp His
725 730 735

Leu Asp Asn His Arg Glu Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro
740 745 750

Ser Glu Lys Arg Gly Glu Leu Asp Asp Pro Glu Pro Arg Glu His Gly
755 760 765

His Ser Tyr Ser Asn Arg Lys Tyr Glu Ser Asp Glu Asp Ser Leu Gly
770 775 780

Ser Ser Gly Arg Val Cys Val Glu Lys Trp Asn Leu Leu Asn Ser Ser
785 790 795 800

Arg Leu His Leu Pro Arg Ala Ser Ala Val Ala Leu Glu Val Gln Arg
805 810 815

Leu Asn Ala Leu Asp Leu Glu Lys Ile Gly Lys Ser Ile Leu Gly
820 825 830

Lys Val His Leu Ala Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys
835 840 845

Glu Lys Gly Glu Glu Trp Asp Gln Glu Ser Ala Val Phe His Leu Glu
850 855 860

His Ala Ala Asn Leu Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu
865 870 875 880

Met Tyr Ser Gln Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys
885 890 895

Glu Thr Glu Glu Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala
900 905 910

Ala Glu Ala Gly Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe
915 920 925

Asp Ser Gly Gln Asn Leu Ser Pro Asp Arg Cys Gln Asp Trp Leu Glu
930 935 940

Ala Leu His Trp Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu
945 950 955 960

Gly Gly Glu Tyr Asp Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu
965 970 975

Ala Arg Glu Ala Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys
980 985 990

Asp Pro Gln Arg Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala
995 1000 1005

Met Glu Ala Met Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys
1010 1015 1020

Ala Glu Glu Ala Trp Ala Gln Met Glu Glu
1025 1030

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<213> Artificial Sequence

<220>
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<400> 7

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<212> PRT
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<400> 8

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
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<210> 9
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<220>
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<222> (2)..(2)
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<400> 9

Asp Xaa Trp Xaa Xaa Gly
1 5